

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: August 21, 2001, 12:07:03 ; Search time 22.69 Seconds
(without alignments)
1830.929 Million cell updates/sec

Title: US-09-486-334-2
Perfect score: 1641
Sequence: 1 MATCIDTCRTGNTQDDSDSR.....IPCLTMDQTSYLEMSDYVI 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-unclassified:*
13: SP-vertebrate:*
14: SP-virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1641	100.0	314	10	Q43297
2	1611	98.2	314	10	Q42588
3	1215	74.0	391	10	Q42532
4	1208	73.6	336	10	Q39218
5	877	53.4	347	10	P93544
6	872	53.1	289	10	Q9MAZ3
7	869	53.0	294	10	Q39533
8	861	52.5	289	10	Q9SDP2
9	849.5	51.8	323	10	Q42538
10	711	43.3	368	10	Q9SRB0
11	699	42.6	315	10	Q9SEB6
12	649.5	39.6	272	2	Q9JRB6
13	647.5	39.5	273	2	Q9KNT2
14	629.5	38.4	402	10	Q9SLZ8
15	610.5	37.2	312	2	Q9L3R1
16	587.5	35.8	299	10	Q9US33
17	587.5	35.8	299	10	Q9US33
18	472.5	28.8	270	2	Q9US33
19	422.5	25.7	227	2	Q32979

20	415.5	25.3	245	2	Q86162	Q86162 synechococ
21	409	24.9	251	2	Q69218	Q69218 azobacter
22	405	24.7	229	2	P95231	P95231 mycobacteri
23	395	24.1	229	2	Q9KGF5	Q9KGF5 bacillus ha
24	392	23.9	258	2	Q9HX16	Q9HX16 pseudomonas
25	391	23.8	243	1	Q9HHA4	Q9HHA4 methanosarc
26	388.5	23.7	212	2	Q9PPF6	Q9PPF6 campylobact
27	378	23.0	191	2	Q9LAR1	Q9LAR1 clostridium
28	370	22.5	265	2	Q44541	Q44541 azobacter
29	338.5	20.6	220	2	Q9WZD4	Q9WZD4 thermotoga
30	312	19.0	171	1	Q9HPT3	Q9HPT3 halobacteri
31	307.5	18.7	305	5	Q9UBX2	Q9UBX2 entamoeba h
32	298	18.2	439	10	Q9M9F2	Q9M9F2 arabidopsis
33	290	17.7	300	5	Q9UBX0	Q9UBX0 entamoeba d
34	287	17.5	305	5	Q9UBX1	Q9UBX1 pseudomonas
35	265	16.1	231	2	Q9I210	Q9I210 salmone
36	263	16.1	162	2	Q9F7A9	Q9F7A9 salmone
37	207	13.0	184	2	Q9KTI3	Q9KTI3 vibrio chol
38	204	12.4	197	2	Q9SV13	Q9SV13 escherichia
39	193	11.8	275	5	Q9GV13	Q9GV13 leishmania
40	184.5	11.2	419	2	Q9RDX7	Q9RDX7 legionella
41	177.5	10.8	143	2	Q9KTH9	Q9KTH9 vibrio chol
42	175	10.7	236	2	Q9XIK7	Q9XIK7 thermotoga
43	175	10.7	240	2	Q9K9H8	Q9K9H8 bacillus ha
44	168	10.2	172	2	Q9XAC2	Q9XAC2 escherichia
45	162.5	9.9	239	2	Q9EZ10	Q9EZ10 staphylococ

ALIGNMENTS

RESULT 1
Q43297 PRELIMINARY: PRT: 314 AA.
AC Q43297;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SERINE O-ACETYLTRANSFERASE)
DE (P14J16.18).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=COLUMBIA;
RC MEDLINE=95154333; PubMed=7851429;
RX Ruffet M.L., Lebun M., Droux M., Douce R.;
RT "Subcellular distribution of serine acetyltransferase from Pisum
RT sativum and characterization of an Arabidopsis thaliana putative
RT cytosolic isoform";
RL Eur. J. Biochem. 227:500-509(1995).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=COLUMBIA;
RC Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP Shinn P., Brooks S., Buehler E., Chao O., Johnson-Hopson C., Khan S.,
RA Kim C., Alfieri H., Bel O., Chin C., Chio J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukhin N., Nguyen M.,
RA Parn C., Pham P., Sakano H., Schwartz J., Soultwick A., Thayer A.,
RA Toriumi M., Vayenberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F14J16 from chromosome
RT 1";
RN Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A.

RA Ecker J.R.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altafi H., Bet B., Chin C., Chlou J., Choi E.,
 RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharly N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Theologis A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 RA Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RL
 CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
 CC SERINE.
 DR EMBL: Z34888; CA84371.1; -;
 DR EMBL: L34076; AA58608.1; -;
 DR EMBL: AC002304; AA79319.1; -;
 DR Mendel: 6701; At4th:1221;6701.
 DR InterPro: IPR001451; -;
 DR Pfam: PF00132; hexapep; 3.
 DR PROSITE: PS00101; HEXAPEP.TRANSFERASES; 1.
 DR Transference: Acyltransferase.
 SQ SEQUENCE 314 AA; 34251 MW; 78ACE3DA5CE04B0 CRC64;

Query Match Best Local Similarity 100.0%; Score 1641; DB 10; Length 314;
 Matches 314; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MATCIDTCRGNTODDDSRCCIKNFRRGFSVNRKIHHTQIEDDDVWIKMLEAKSDV 60
 DB 1 MATCIDTCRGNTODDDSRCCIKNFRRGFSVNRKIHHTQIEDDDVWIKMLEAKSDV 60
 OY 61 KQPIILSNYYASITSHRSLSALAHILSVKLSNLPNSNLFELFISVLEESPEIEST 120
 DB 61 KQPIILSNYYASITSHRSLSALAHILSVKLSNLPNSNLFELFISVLEESPEIEST 120
 OY 121 KODLIAKKEPDACISYVHCFGLGKFLACQAHRIATLTKONRKIVALLIONRSESFA 180
 DB 121 KODLIAKKEPDACISYVHCFGLGKFLACQAHRIATLTKONRKIVALLIONRSESFA 180
 OY 181 VDIHPGAKIGKILIDHATGVVIGETAVGDNVSIHGVTLGGTGKSGDRPKIGDYL 240
 DB 181 VDIHPGAKIGKILIDHATGVVIGETAVGDNVSIHGVTLGGTGKSGDRPKIGDYL 240
 OY 241 IGAGSCIIGNITTEGAKIGSGSVYVNDVARTAVGNPARKLIGKENPRKHDKIPCLTM 300
 DB 241 IGAGSCIIGNITTEGAKIGSGSVYVNDVARTAVGNPARKLIGKENPRKHDKIPCLTM 300
 OY 301 DOTSTLTMSDYVI 314
 DB 301 DOTSTLTMSDYVI 314
 RESULT 2
 ID 042588 PRELIMINARY; PRT; 314 AA.
 AC 042588;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)

DE SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SERIII, O-ACETYLTRANSFERASE).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Murillo M., Foglia R., Diller A., Leustek T.;
 RL Cell. Mol. Biol. Res. 0:0-0(0).
 CC -1- CATALYTIC ACTIVITY: ACETYL-COA + L-SERINE = COA + O-ACETYL-L-
 CC SERINE.
 DR EMBL: L42212; AAC37474.1; -;
 DR Mendel: 6700; At4th:1221;6700.
 DR InterPro: IPR001451; -;
 DR Pfam: PF00132; hexapep; 3.
 DR PROSITE: PS00101; HEXAPEP.TRANSFERASES; 1.
 DR Transference: Acyltransferase.
 SQ SEQUENCE 314 AA; 34259 MW; A096DF6D2768E21C CRC64;

Query Match Best Local Similarity 98.2%; Score 1611; DB 10; Length 314;
 Matches 308; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 MATCIDTCRGNTODDDSRCCIKNFRRGFSVNRKIHHTQIEDDDVWIKMLEAKSDV 60
 DB 1 MATCIDTCRGNTODDDSRCCIKNFRRGFSVNRKIHHTQIEDDDVWIKMLEAKSDV 60
 OY 61 KQPIILSNYYASITSHRSLSALAHILSVKLSNLPNSNLFELFISVLEESPEIEST 120
 DB 61 KQPIILSNYYASITSHRSLSALAHILSVKLSNLPNSNLFELFISVLEESPEIEST 120
 OY 121 KODLIAKKEPDACISYVHCFGLGKFLACQAHRIATLTKONRKIVALLIONRSESFA 180
 DB 121 KODLIAKKEPDACISYVHCFGLGKFLACQAHRIATLTKONRKIVALLIONRSESFA 180
 OY 181 VDIHPGAKIGKILIDHATGVVIGETAVGDNVSIHGVTLGGTGKSGDRPKIGDYL 240
 DB 181 VDIHPGAKIGKILIDHATGVVIGETAVGDNVSIHGVTLGGTGKSGDRPKIGDYL 240
 OY 241 IGAGSCIIGNITTEGAKIGSGSVYVNDVARTAVGNPARKLIGKENPRKHDKIPCLTM 300
 DB 241 IGAGSCIIGNITTEGAKIGSGSVYVNDVARTAVGNPARKLIGKENPRKHDKIPCLTM 300
 OY 301 DOTSTLTMSDYVI 314
 DB 301 DOTSTLTMSDYVI 314

RESULT 3
 ID 042532 PRELIMINARY; PRT; 391 AA.
 AC 042532; Q43740; Q43739;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE SERINE O-ACETYLTRANSFERASE (EC 2.3.1.30) (SERINE O-ACETYLTRANSFERASE)
 GN SAT-1 OR SAT A.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA MEDLINE=96270381; PubMed=8639741;
 RA Roberts M.A., Wray J.L.;
 RT Cloning and characterization of an Arabidopsis thaliana cDNA clone
 encoding an organellar isoform of serine acetyltransferase.*;

DR EMBL: D88530; BAA13635.1; -
 DR EMBL: D88529; BAA13634.1; -
 DR Mendel: 10792; Spol:1221;10792.
 DR InterPro: IPR001451; -
 DR Pfam: PF00132; hexapep; 3.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
 KW Transferrase.
 SQ SEQUENCE 347 AA; 37256 MW; FBAB365488DB60E CRC64;

Query Match 53.4%; Score 877; DB 10; Length 347;
 Best Local Similarity 56.6%; Pred. No. 2.9e-63;
 Matches 163; Conservative 53; Mismatches 70; Indels 2; Gaps 1;

QY 29 PG-FSVNRKIHHTQIEDDDWIKMLEKASDVKEPILSNYYASTSHRSLESALAH 86
 DB 60 PGGLSVAPSVGLHANNEMIMDQIKGRADSEPALASYLSTILSHSLERSLSF 119
 QY 87 ILVKSILNLPSTLFEFTSVLESPETESTKODLAVKRPACISYVHCFLGFKG 146
 DB 120 HLGKSLCSSTLLSTLYDLFLNLSSDSSILDVAADLAARVPACVSHCLNKG 179
 QY 147 FLACQARIATLMKONRKIVALLLIONRVSEFAVDHHPGAKIGKILDHATGVIGET 206
 DB 180 FLACQSHRAVAKLMODRPRALALHSRISDFAVDHPARIGKILFDHATGVIGET 239
 QY 207 AVAGDVSILHGTGCTGKSGDNHPKIGDGVLLGAGSCILGNITIGEGAKIGSGSVV 266
 DB 240 AIIIGDCSILHVTLLGCTGKAGDRHPYGDGVLLGAGATILGNVRIGDGAIGAGSVVL 299
 QY 267 KDVPARTAVGNPARLIGKENRPHKDKIPCLTMDQTSYLTENSDYIT 314
 DB 300 IDVPRTAVGNPARLIGKEKPSQNSDVPESMDHTSFISEMSDYIT 347

RESULT 6
 O9MAZ3 PRELIMINARY; PRT; 289 AA.
 AC O9MAZ3;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE SERINE ACETYLTANSFERRASE.
 GN ASAT5.
 OS Allium tuberosum.
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 CC Magnoliophyta; Liliopsida; Asparagales; Alliaceae; Allium.
 RN NCBL_TaxID=4683;
 RP SEQUENCE FROM N.A.
 RA Urano Y., Saito K.;
 RT "Allium tuberosum mRNA for serine acetyltransferase";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB040502; BAA93050.1; -
 DR InterPro: IPR001451; -
 DR Pfam: PF00132; hexapep; 3.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
 KW Transferrase.
 SQ SEQUENCE 289 AA; 30671 MW; 60C2D784D25CF383 CRC64;

Query Match 53.1%; Score 872; DB 10; Length 289;
 Best Local Similarity 61.3%; Pred. No. 5.7e-63;
 Matches 166; Conservative 43; Mismatches 62; Indels 0; Gaps 0;

QY 44 DDDWIKMLEKASDVKEPILSNYYASTSHRSLESALAHILSKSNLNPSTLFE 103
 DB 19 DSSWVWNIKAEARDASEPALASYLSTILSHPLANSLANKLCSSTLSTLSY 78
 QY 104 ELFTSVLESPETESTKODLAVKRPACISYVHCFLGFKGFLACQARIATLMKON 163
 DB 79 DLFLNASTFTLISATVADILAHARHPACIGSHCLNFKGLAVVQRIAHVLMGQS 138

QY 164 RTIYALLIONRVSEFAVDHHPGAKIGKILLDHATGVY3ETAVGDNVSLHGTG 223
 DB 139 RRPALALHSRVADVSLVHPARIGKILLDHATGVY3ETAVGNVSLHHTLGG 198
 QY 224 TKGSDRHPKIGDGVLLGAGSCILGNITIGEGAKIGSGSVVVDVPAARTAVGNPARLI 283
 DB 199 TKGAGDRHPKIGDGVLLGAGATILGNIRIGAGAKIGAGSVLLIDVPPRTAVGNPARLI 258
 QY 284 GKENRPHKDKIPCLTMDQTSYLTENSDYIT 314
 DB 259 GKENRPHMEDVPGESMDHTSFISEMSDYIT 289

RESULT 7
 O39533 PRELIMINARY; PRT; 294 AA.
 AC O39533; O04734;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE SERINE ACETYLTANSFERRASE.
 GN SAT.
 OS Citrullus lanatus (Watermelon) (Citrullus vul. varis).
 CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Cucurbitales; Cucurbitaceae; Citrullus.
 RN NCBL_TaxID=3654;
 RP SEQUENCE FROM N.A.
 RA Saito K., Inoue K., Fukushima R., Noji M.;
 RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-KINRO; TISSUE=GREEN LEAVES;
 RX MEDLINE=95332343; PubMed=7608200;
 RA Saito K., Yokoyama H., Noji M., Murakoshi I.;
 RT "Molecular cloning and characterization of a plant serine acetyltransferase playing a regulatory role in cysteine biosynthesis from watermelon";
 RL J. Biol. Chem. 270:16321-16326 (1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-KINRO;
 RA Noji M., Inoue K., Saito K.;
 RT Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: D85624; BAA12843.1; -
 DR EMBL: D49535; BAA08479.1; -
 DR EMBL: AB006530; BAA21827.1; -
 DR Mendel: 7748; Cila:1221;7748.
 DR InterPro: IPR001451; -
 DR Pfam: PF00132; hexapep; 3.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
 KW Transferrase.
 SQ SEQUENCE 294 AA; 31537 MW; D9BA9667F638F8D CRC64;

Query Match 53.0%; Score 869; DB 10; Length 294;
 Best Local Similarity 58.6%; Pred. No. 1e-62;
 Matches 163; Conservative 49; Mismatches 66; Indels 0; Gaps 0;

QY 37 IHTQIEDDDWIKMLEKASDVKEPILSNYYASTSHRSLESALAHILSKSNLNPSTLFE 103
 DB 17 VESTNNDETWMGQIKAEARDASEPALASYLSTILSHSLERSLSHLNKLCSST 76
 QY 97 LPSTLFEFTSVLESPETESTKODLAVKRPACISYVHCFLGFKGFLACQARIATLMKON 163
 DB 77 LLSTLYDLFLNASTFTVCLRSVAVADLAARERDPACVSHCLNFKGLAVVQRIAHVLMGQS 138
 QY 157 HTLMKONRKIVALLLIONRVSEFAVDHHPGAKIGKILLDHATGVYIGETAVGDNVSL 216
 DB 137 HKLMGSRRLALALQSRILADVFAVDHHPARIGKILFDHATGVYIGETAVGDNVSL 196

Oy	217	HGYLIGCTKQSGDHPRIIGDGVILGAGSCILNITTEGAKIGSGSVVKKVPARTTAV	276
Db	197	HHVTLLGTGCKMGCDHPRPIGDGVILGAGATTLGNVKIGESAKIGAGSVLLIDVPPRTTAV	256
Oy	277	GNPRLIGKENPRKHDKIPCLTMDQTSYLTWMSDYII	314
Db	257	GNPRLVGKEKRPSQLEDIPGSMDHSTFISEMSDYII	294
RESULT	8		
Q9SDP2			
ID	Q9SDP2	PRELIMINARY:	PRT: 289 AA.
AC	Q9SDP2:		
DT	01-MAY-2000 (TREMBLrel. 13, Created)		
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)		
DE	SERINE ACETYLTRANSFERASE.		
OS	Allium cepa (Onion).		
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
OC	Magnoliophyta; Liliopsida; Asparagales; Alliaceae; Allium.		
CX	NBI_TaxID=4679;		
RA	(1)		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-CV. PUKROHE LONG KEEPER; TISSUE-ROOT;		
RA	Pither-Joyce M.D., McCallum J.A.;		
RT	"Isolation of a serine acetyltransferase cDNA clone from Allium		
RT	cepa ";		
RL	Submitted (DEC-1989) to the EMBL/GenBank/DBJ databases.		
DR	EMBL, AF212156; AAF19000.1; -.		
DR	InterPro: IPR001451; -.		
DR	Pfam: PF001132; hexapep. 3.		
DR	PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.		
KM	Transferrase.		
SQ	SEQUENCE 289 AA; 30574 MW; 9EA376C54DA0AFl3 CRC64;		
Query Match	52.5%; Score 861; DB 10; Length 289;		
Best Local Similarity	59.8%; Pred. NO. 4.4e-62;		
Matches 162; Conservative	46; Mismatches 63; Indels 0; Gaps 0		
Oy	44	DDDDWIKMLEEAKSDVKOEPIILSYNYYSITSHSLSALAHILSVLSMLNLPSTLTF	103
Db	19	DESVMWNQIKRAHRKDSEPALASLYTITSHRSLSARSLSPHLANKLCSSTLLSTSLY	78
Oy	104	ELFTSVLEESPETTESTKODLIAVKERDPACISVYNCHFLGRKGFLIACAHAIAATLTKON	163
Db	79	DLFLTTLSTFFPTVSASADVADLIARHRDCAVCFSHCLNFEGFLAVTORIAIVLMQS	138
Oy	164	RKIYVALLQNVSFSPAVDTHPGAKIGKGLLDHATGVYIGFTAVVGNVSIHGVTLGG	223
Db	139	RRLPALAHSNVAVDLSVDIHPARIGKGLLDHATGVYIGETVAIGNNVSIHHVTLGG	198
Oy	224	TGKQSGDHPRIIGDGVILGAGSCILNITTEGAKIGSGSVVKKVPARTTAGNPARLI	283
Db	199	TGKAGGDHPRIIGDGVILGAGATTLGNIRIGAKVAGKAGSVLLIDVPPRTTAGNPARLI	258
Oy	284	GGENPRKHDKIPCLTMDQTSYLTWMSDYII	314
Db	259	GGEKRPVYHEDVPGESMDHTSFISEMSDYII	289
RESULT	9		
Q4Z538			
ID	Q4Z538	PRELIMINARY:	PRT: 312 AA.
AC	Q4Z538:		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)		
DE	SERINE ACETYLTRANSFERASE (EC 2.3.1.30) (SERINE O-ACETYLTRANSFERASE)		
DE	*SERINE O-ACETYLTRANSFERAS (EC 2.3.1.30) SAT-52).		
GN	SAT-52.		
OS	Arabidopsis thaliana (Mouse-ear cress);		
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		

CC Magnoliophyta: eudicotyledons, core eudicots, Rosidae, eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RX MEDLINE=98403884; PubMed=9048879;
RA Howarth J.R., Roberts M.A., Wray J.L.;
RT "Cysteine biosynthesis in higher plants: a new member of the
RT Arabidopsis thaliana serine acetyltransferase small gene-family
RT obtained by functional complementation of an Escherichia coli cysteine
RT auxotroph";
RL Biochim. Biophys. Acta 1350:123-127(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RX MEDLINE=98403884; PubMed=9734815;
RA Kocani H., Nakamura Y., Sato S., Asamizu E., Kaneo T., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI,
RT Sequence/features of the regions of 1,367,185 bp covered by 19
RT physically assigned pl and TAC clones.";
RL DNA Res. 5:203-216(1998).
DR EMBL; U30298; AAC49655.1; -
DR EMBL; AB013392; BAB09894.1; -
DR Mendel; 6699; Arath;1221;6699.
DR InterPro; IPR001451; -
DR Pfam; PF00132; hexapep; 3.
DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
KW transferase, Acyltransferase.
SQ Transferrase 312 AA; 32770 MM; 15835510FFJ14A.3 CRC64;

Query Match 51.8%; Score 849.5; DB 10; Length 312;
Best Local Similarity 59.7%; Pred. No. 4.2e-61;
Matches 160; Conservative 45; Mismatches 12; Indels 1; Gaps 1.

OY 48 VWIKLEAKSKDVKQEPILSNYYASTSHRSLESMLHLSVKSLSNLPNSMTLFELFI 107
 ::: :::: :|| :::: ||| :::: |:: :::
DB 45 LWTQIAARRDAERPAALSYLTSLHSLSERSISIFGHNKICSSLTSLTLTYDLFL 104
 ::: :::: :|| :::: ||| :::: |:: :::
OY 108 SVLESPELTSTKODLIAYKERDPACISYVHCFLFKGLACQAHRIATHTLMKNRKIV 167
 ::: :::: :|| :::: ||| :::: |:: :::
DB 105 NFPSDSPSLRATYAADLRARVRNPACISPHCLNLNYKGLAIQHVRSHKLMTQSRRPL 164
 ::: :::: :|| :::: ||| :::: |:: :::
OY 168 ALLIGNRVSESFANDIHFGAKTIGILLDTATGVYIGETFAVVGDNVSTLHGVTGGTGKQ 227
 ::: :::: :|| :::: ||| :::: |:: :::
DB 165 ALATHSRISIDFVAVDIHPAAKTIGILLDTATGVVGTETLGNVNSTLHHVTTLGCTGKA 224
 ::: :::: :|| :::: ||| :::: |:: :::
OY 228 SGDRHKTKGGDVLGAGSCIIINTTIGEGAKTIGSGSVVWLNPARTTVGNPARLIGKE 287
 ::: :::: :|| :::: ||| :::: |:: :::
DB 225 CGGRHKTKIGDGCLLAGACTITLGNKTIAGAKVAGSGVLLVPFGSTAVGNPARLVGKE 284
 ::: :::: :|| :::: ||| :::: |:: :::
OY 288 NPRKHD-KIPCLTMDDTSYLTWMSDYVI 314
 ::: :::: :|| :::: ||| :::: |:: :::
DB 285 KPTIHDECPGESMDHTSFISEMSDYII 312

RESULT 10
ID Q9ZPJ4 PRELIMINARY; PRT; 323 AA.
AC Q9ZPJ4;
DC 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
GN SAT-106.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Howarth J.R., Roberts M.A., Wray J.L.;
 RT "A fourth member of the serine acetyltransferase gene-family from
 Arabidopsis thaliana";
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF112303; AAD19965.1;
 DR InterPro: IPR001451;
 DR Pfam: PF00132; hexaped; 2.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
 DR Transferrase: Acyltransferase.
 SO SEQUENCE 323 AA; 34534 MM; 8CE538962B44E610 CRC64;

Query Match 43.3%; Score 711; DB 10; Length 323;
 Best Local Similarity 50.5%; Pred. No. 7, 7e-50;
 Matches 141; Conservative 48; Mismatches 78; Indels 12; Gaps 3;

QY 27 FRPGSVNKK-IHHQIEDD-----DDWIKMLEAKSDVKQEPILSNYYASITSHRS 79
 DB 8 FESGEVYAKGTHKSEFDSNLDPRSDPIWDAIREAKLEAKKEPILSFLYAGIILAHDC 67
 QY 80 LESALHILSVKLSNLTPELFSVLEESPEITESTKODLIIVKEDRPACTSYH 139
 DB 68 LEQALGFVLANKLONPTLLATQLDIFYGVMHDKGIQSSIRHDLQAFKDRDPACLSYSS 127
 QY 140 CFLGKGFACQAHRIAHITLTKONKRIYALLIONRVSESPAVNDIHPGAKIGKILDHAT 199
 DB 128 AILHLKGYHALQAVYARVAKHKNNEGRKLLALQSRISVEGDIHPAPRIGEGILDHGT 187
 QY 200 GVIGETAVGDNVSIILHGVTILGCTGKOSGRHPRKIGDGVILGAGSCIIGNITIGGAKI 259
 DB 188 GVIGETAVIGNVSIILHGVTILGCTGKEDRHRPKIGEGALACVITLIGNISIGAGAVY 247
 QY 260 GSGSVYKDVARTAVANGPARLIGKEN-----PRKHD 293
 DB 248 AAGSLVLKDVPSHVSVAQNPAKLIRWEEDPDLAMKHD 286

RESULT 11
 ID Q9STB0 PRELIMINARY; PRT; 368 AA.
 AC Q9STB0;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
 DE SERINE ACETYLTRANSFERASE 2.
 GN SAT2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Ruffet M.-L., Lebun M., Droux M., Douce R.;
 RT "Gene sequence of serine acetyltransferase 2 from A. thaliana";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: L78444; AAD5614.2;
 DR InterPro: IPR001451;
 DR Pfam: PF00132; hexaped; 2.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
 SO SEQUENCE 368 AA; 39575 MM; 84BC037D15FCASCE CRC64;

Query Match 43.3%; Score 711; DB 10; Length 368;
 Best Local Similarity 50.5%; Pred. No. 9, 3e-50;
 Matches 141; Conservative 48; Mismatches 78; Indels 12; Gaps 3;

QY 80 LESALHILSVKLSNLTPELFSVLEESPEITESTKODLIIVKEDRPACTSYH 139
 DB 113 LEQALGFVLANKLONPTLLATQLDIFYGVMHDKGIQSSIRHDLQAFKDRDPACLSYSS 172
 QY 140 CFLGKGFACQAHRIAHITLTKONKRIYALLIONRVSESPAVNDIHPGAKIGKILDHAT 199
 DB 173 AILHLKGYHALQAVYARVAKHKNNEGRKLLALQSRISVEGDIHPAPRIGEGILDHGT 232
 QY 200 GVIGETAVGDNVSIILHGVTILGCTGKOSGRHPRKIGDGVILGAGSCIIGNITIGGAKI 259
 DB 233 GVIGETAVIGNVSIILHGVTILGCTGKEDRHRPKIGEGALACVITLIGNISIGAGAVY 292
 QY 260 GSGSVYKDVARTAVANGPARLIGKEN-----PRKHD 293
 DB 293 AAGSLVLKDVPSHVSVAQNPAKLIRWEEDPDLAMKHD 331
 RESULT 12
 ID Q9SEY6 PRELIMINARY; PRT; 315 AA.
 AC Q9SEY6;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
 DE PURATIVE SERINE ACETYLTRANSFERASE.
 GN AT2G17640.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Beato M.-I., Town C.D.,
 RA Buell C.R., Mason T.M., Bowman C.L., Barnstead J.M.E., Feldblyum T.V.,
 RA Cronin L.A., Shen M., VanKien S.E., Umayam L., Patton L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome II of Arabidopsis thaliana";
 RL Nature 402:761-768(1999).
 DR EMBL: AF024504; AAF18673.1;
 DR InterPro: IPR001451;
 DR Pfam: PF00132; hexaped; 2.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERASES; 1.
 DR Transferrase.
 SO SEQUENCE 315 AA; 34000 MM; FD15AC3EBA150B2F CRC64;

Query Match 42.6%; Score 699; DB 10; Length 315;
 Best Local Similarity 50.2%; Pred. No. 7e-49;
 Matches 141; Conservative 50; Mismatches 76; Indels 14; Gaps 4;

QY 27 FRPGSVNKK-IHHQIEDD-----DDWIKMLEAKSDVKQEPILSNYYASITSHRS 79
 DB 8 FESGEVYAKGTHKSEFDSNLDPRSDPIWDAIREAKLEAKKEPILSFLYAGIILAHDC 65
 QY 80 LESALHILSVKLSNLTPELFSVLEESPEITESTKODLIIVKEDRPACTSYH 139
 DB 66 LEQALGFVLANKLONPTLLATQLDIFYGVMHDKGIQSSIRHDLQAFKDRDPACLSYSS 125
 QY 140 CFLGKGFACQAHRIAHITLTKONKRIYALLIONRVSESPAVNDIHPGAKIGKILDHAT 199
 DB 126 AILHLKGYHALQAVYARVAKHKNNEGRKLLALQSRISVEGDIHPAPRIGEGILDHGT 185
 QY 200 GVIGETAVGDNVSIILHGVTILGCTGKOSGRHPRKIGDGVILGAGSCIIGNITIGGAKI 259
 DB 186 GVIGETAVIGNVSIILHGVTILGCTGKEDRHRPKIGEGALACVITLIGNISIGAGAVY 245

OY 260 GSGSVVVDVAVTAVGNPARKLIGKGNPRKDKIPCLTM 300
 :||:||||: : ||||| : : : : :
 Db 246 AAGSLVAKDVPVSHSVAGNPAKLIRVME-----EDDPSLAM 281

RESULT 13

09JUR86 PRELIMINARY: PRT: 272 AA.
 AC 09JUR86;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
 DE PUTATIVE SERINE ACETYLTRANSFERASE (EC 2.3.1.30).
 GN CSE OR NMA0742 OR NMB0560.
 OS Neisseria meningitidis (serogroup A), and
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=65699, 491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;
 RX MEDLINE=20222556; PubMed=10761919;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
 Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 Davies R.M., Davis P., Devlin K., Felwell T., Hamlin N., Holroyd S.,
 Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
 Rajadream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 Whitehead S., Spratt B.G., Barrall B.G.,
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 meningitidis 22491."
 RL Nature 404:502-506(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MC58 / SEROGROUP B;
 RX MEDLINE=20175753; PubMed=10710307;
 RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 Eisten J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 Nelson M.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
 Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 Mason T., Clecke A., Parkey D.S., Blair E., Ciltone H., Clark E.B.,
 Cotton M.D., Uitterback T.R., Khouli H., Qin H., Vamathevan J.,
 Gill J., Scarlato V., Masignani V., Piza M., Grandi G., Sun L.,
 Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 MC58."
 RL Science 287:1809-1815(2000).
 DR EMBL: AL162754; CAB84026.1;
 DR EMBL: AE002412; AAF40988.1;
 DR TIGR: NMB0560;
 DR InterPro: IPR001451;
 DR Pfam: PF00132; hexapep. 3.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
 DR Transferrase; Acyltransferase.
 KW KW
 SQ SEQUENCE 272 AA; 29399 MW; 4CB7AD8A916386EB CRC64;

Query Match 39.6%; Score 649.5; DB 2; Length 272;

Best Local Similarity 50.7%; Pred. No. 5.9e-45;

Matches 136; Conservative 39; Mismatches 86; Indels 7; Gaps 2;

OY 47 DWIMKLEAKSDVKEPILSNYYASITSHRSLESALAHILSVKLSNLPNTLFEF 106
 :||:||||: : ||||| : : : : :
 Db 12 DLWHTIRETAATAVSAEPMLASFLHQTALRHESLSVLAHLSKLSPLIDVRALEF 71
 OY 107 ISVLESPEIISTKODLIANKERDPACISVHCFGLGFKGLACQAHRIANTLTKOKRKI 166
 :||:||||: : ||||| : : : : :
 Db 72 QOALGSDTQIGKVCADKAIEKDPACDEYSLPLYKGFHAIQAHRIANTLILDRKKT 131
 OY 167 VALLIGNRSEFAVDIHPGAKIGKIGLLDHAITGVIGETAVGDNVSIHLGVTLGSTGK 226
 :||:||||: : ||||| : : : : :
 Db 132 IATFLONRSEYFQVDIHPAARFGVIMDHAITGVAVETAVLGNNISILHGVTLGSGK 191
 OY 227 QSGDRHPKIGDVLIGAGSCILGNITIGBGAKIGSGSVVVDVAVTAVGNPARKLIGK 286

Db 192 EGGDRHPKIGDVGWIGANNSILGNIRIGSNAKIGAGSVVSDVPSTIVGVPKPAVA-- 249
 OY 287 ENPRKDKIPCLTMDQTSYLTWESDVI 314
 Db 250 ----RSLKTPSADMDONIQFTE-IDPMI 272

RESULT 14

09KNT2 PRELIMINARY: PRT: 273 AA.
 AC 09KNT2;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, last sequence update)
 DE PUTATIVE SERINE ACETYLTRANSFERASE.
 GN VC2649.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrrio.
 OX NCBI_TaxID=665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EL TOR N16961 / SEROTYPE O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisten J.A., Nelson W.C., Cotton R.A., Gwinn M.L.,
 Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,
 McDonald L., Uitterback T., Fleischmann R.D., Newman W.C., White O.,
 Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae."
 RL Nature 406:477-483(2000).
 DR EMBL: AE004331; AAF95790.1;
 DR TIGR: VC2649;
 DR InterPro: IPR001451;
 DR Pfam: PF00132; hexapep. 4.
 DR PROSITE: PS00101; HEXAPEP_TRANSFERRASES; 1.
 DR Transferrase.
 KW KW
 SQ SEQUENCE 273 AA; 29278 MW; 5CBE16376B45B76F CRC64;

Query Match 39.5%; Score 647.5; DB 2; Length 273;

Best Local Similarity 50.0%; Pred. No. 8.7e-45;

Matches 132; Conservative 50; Mismatches 71; Indels 11; Gaps 3;

OY 39 HTQIEDDDDWIMKLEAKSDVKEPILSNYYASITSHRSLESALAHILSVKLSNLP 98
 :||:||||: : ||||| : : : : :
 Db 6 HTK-----VWQTYAARKEQAEDEPMLASTYATITIKHSLAAALSYILANLNASMP 59
 OY 99 SNTLEFISVLESPEIISTKODLIANKERDPACISVHCFGLGFKGLACQAHRIANT 158
 :||:||||: : ||||| : : : : :
 Db 60 AMAVREVEIEFAADPSTSEAAACDICTATVNRDPVAMYSMPLLYKGFHALGQYAVAW 119
 OY 159 LMKONRKIVALLIGNRSEFAVDIHPGAKIGKIGLLDHAITGVIGETAVGDNVSIHLG 218
 :||:||||: : ||||| : : : : :
 Db 120 LMRQGRKALATYFQNOISVACQVDIHPAARFGVIMDHAITGVIGETAVGDNVSIHLG 179
 OY 219 VTLGSGKOSGDRHPKIGDVLIGAGSCILGNITIGBGAKIGSGSVVVDVAVTAVGN 278
 :||:||||: : ||||| : : : : :
 Db 180 VTLGSGKECGDRHPKIEGVWIGAKIILNIEVGBGAKIGSGSVVLAQVPPHTVAGV 239
 OY 279 PARLIGKGNPRKDKIPCLTMDQ 302
 :||:||||: : ||||| : : : : :
 Db 240 PARIVGRPOS----DK-PSLMDQ 258

RESULT 15

09SLZ8 PRELIMINARY: PRT: 402 AA.
 AC 09SLZ8;
 DT 01-MAY-2000 (TREMblrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE SERINE ACETYLTRANSFERASE.
GN CMSAT.
OS Cyanidioschyzon merolae.
OC Eukaryota; Rhodophyta; Bangiophyceae; Cyanidioschyzon.
OX NCBI_TaxID=45157;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98288115; PubMed=9622597;
RA Toda K., Takano H., Miyagishima S., Kuroiwa H., Kuroiwa T.;
RT "Characterization of a chloroplast isoform of serine acetyltransferase
from the thermo-acidophilic red alga Cyanidioschyzon merolae.";
RL Biochim. Biophys. Acta 1403:72-84(1998).
DR EMBL; AB008428; BAA8412.1; .
KW Transferase.
SQ SEQUENCE 402 AA; 43739 MW; D97E69BFF79F452 CRC64;

Query Match 38.4%; Score 629.5; DB 10; Length 402;
Best Local Similarity 47.1%; Pred. No. 4.3e-43;
Matches 130; Conservative 51; Mismatches 92; Indels 3; Gaps 2;

OY 27 FRPGSVNRKIHHTQIEDDDVIMLEAKSDVKQEPILSNYYASITSHRSLESALAH 86
DB 97 FGPVIVSDDMV-RTLTYSDDPMELVREAEIGANEPQLASLYATVLNHRCLEDTLAF 155
OY 87 ILTVKLSNLNPSNTLPELFISVLESPETIESTKODLIANKERDPACISYVHCFGLFGK 146
DB 156 HLANELASPFQAOYVYKLFQDALYODKSYREAIRADLLAVVRDPAMKHCVAVLWYSG 215
OY 147 FLACQAHRIHTLTKONKRIYALLIONRVSSEFAVDIHGAKIGKILLDHATGVIGET 206
DB 216 YAAIQAYRLAHLWQDKVLAFLQSEISKCFADVDIRPARIGSGVMIDHATGIVIGET 275
OY 207 AVGDNVSLILGVTLGIGKSGDRHRKIGDGVILGAGSCLIGNITTEGAKIGSGSVV 266
DB 276 AVGNDVSMILHNTVLGGTGKAGDRHPRKVGKGVLLGAGATVIGNIRIGDGAQITASSVL 335
OY 267 KDVPARTAVGNPARLIGKENPRKHDKIPCLTMDQ 302
DB 336 KDVPPTIVSGVPAREVYKLSYRK--GVYPAFEMDQ 369

Search completed: August 21, 2001, 12:10:05
Job time: 182 sec